

A

GI State

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Find (Accessions, GI numbers or Fasta style Seq/ids) AL162497						<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
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 difference between I and II as GenBank/GenPept

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## Revision history for AL162497

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✓ = 143 + 04 pp

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Accession AL162497 was first seen at NCBI on Mar 29 2000 11:12 PM

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Find (Accessions, GI numbers or Fasta style SeqIds) XM\_007095

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## Sequence Revision History

Search for Genes

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Calculator of orthologous genes

Protein resource on the Web

### Revision history for XM\_007095

This record was removed as a result of standard genome annotation processing. See the genome build documentation at <http://www.ncbi.nlm.nih.gov/genome/guide/build.html> for further information, or contact [Info@ncbi.nlm.nih.gov](mailto:Info@ncbi.nlm.nih.gov).

GI	Version	Update Date	Status	I	II
20545806	6	Apr 28 2003 1:32 PM	Suppressed	C	C
20545806	6	Apr 10 2003 3:18 PM	Dead	C	C
20545806	6	Jan 5 2003 12:07 AM	Dead	C	C
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20545806	6	May 13 2002 4:35 PM	Dead	C	C
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14752884	4	Oct 16 2001 10:26 PM	Dead	C	C
14752884	4	Aug 27 2001 4:37 PM	Dead	C	C
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13627469	3	Apr 17 2001 4:19 PM	Dead	C	C
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12737962	2	Feb 10 2001 3:10 AM	Dead	C	C
11433661	1	Nov 29 2000 3:54 PM	Dead	C	C

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- Search History will be lost after eight hours of inactivity.
- Search numbers may not be continuous; all searches are represented.
- To save search indefinitely, click query # and select Save in My NCBI.
- To combine searches use #search, e.g., #2 AND #3 or click query # for more options.

Search	Most Recent Queries	Time	Result
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	#6 Search granulocyt* AND vesnarinone	09:39:32	11
	#5 Search Hasegawa K AND granulocyt*	09:38:23	7
	#4 Search Hasegawa K	09:38:09	1650
	#3 Search Suematsu K AND granulo*	09:37:31	0
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	#1, Search Suematsu K	09:37:03	67



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gi|20545806|ref|XM\_007095.6|
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Comment Features Sequence
[BLAST](#)

LOCUS XM\_007095 6997 bp mRNA
[Find regions of similarity between this sequence and other sequences using BLAST.](#)

linear PRI 26-APR-2003
[Pick Primers](#)

DEFINITION Homo sapiens insulin receptor substrate 2 (IRS2), mRNA.
[Design and test primers for this sequence using Primer-BLAST](#)

ACCESSION XM\_007095
[Recent Activity](#)

VERSION XM\_007095.6 GI:20545806
[Turn Off](#) [Clear](#)

KEYWORDS
gi|20545806|ref|XM\_007095.6|

SOURCE Homo sapiens (human)
[XM\\_007095.1](#)
[Nucleotide](#)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata;

Vertebrates; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 6997)

AUTHORS International Human Genome Sequencing Consortium.

TITLE The DNA sequence of Homo sapiens

JOURNAL Unpublished (2003)

COMMENT MODEL\_PSEQ: This record is predicted by automated computational analysis. This record is derived from a genomic sequence

(NT\_009952) annotated using gene prediction method: BLAST,

supported by mRNA and EST evidence.

Also see:

[Documentation of NCBI's Annotation Process](#)

On May 13, 2002 this sequence version replaced

gi:18581715.

FEATURES Location/Qualifiers

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 4981 agtcccttaccat cttttttttt tttttttttt tttttttttt tttttttttt  
 5041 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
 5101 agtagacacg tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
 5161 gccccggggcc gggactttttt tttttttttt tttttttttt tttttttttt tttttttttt  
 5221 gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
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 5461 cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
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 6721 acctttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
 6781 aatgttgcata aaaaatccgg tttttttttt tttttttttt tttttttttt tttttttttt  
 6841 cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
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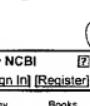
//

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GenBank: AL162497.20

## Human DNA sequence from clone RP11-313L9 on chromosome 13 Contains a novel gene, the IRS2 gene for insulin receptor substrate 2 and two CpG islands, complete sequence

Comment Features Sequence

LOCUS AL162497 143409 bp DNA  
 linear PRI 13-JAN-2009  
 DEFINITION Human DNA sequence from clone RP11-313L9 on chromosome 13 Contains a novel gene, the IRS2 gene for insulin receptor substrate 2 and

two CpG islands, complete sequence.

ACCESSION AL162497  
 VERSION AL162497.20 GI:14329908  
 KEYWORDS HTG; CpG island; insulin receptor; IRS2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata;  
 Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates;

Haplorrhini;  
 Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (based 1 to 143409).  
 AUTHORS Mashreghi-Mohammadi, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-JAN-2009) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk  
 COMMENT Clone requests: Geneservice (<http://www.geneservice.co.uk/>) and BACPAC Resources (<http://bacpac.chori.org/>)  
 gi:14280409. On Jun 8, 2001 this sequence version replaced

----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: vega@sanger.ac.uk  
 -----  
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by

Change Region Shown

Customize View

Sequence Analysis Tools

BLAST Sequence

Pick Primers

Homologs of IRS2

The IRS2 gene is conserved in chimpanzee, dog, mouse, rat, chicken, and zebrafish.

Recent Activity

Human DNA sequence from clone

AL162497 (1) Nucleotide

metalloproteinase [Cnidaria fasciculata]

162497 (0) Nucleotide

GenBank

All links from this record

Assembly

Gene

Gene Genotype

GeneView in dbSNP

Genome Project

Protein

PubMed (Weighted)

Taxonomy

Related Sequences

Map Viewer

OMIM

restriction digest,  
     except on the rare occasion of the clone being  
     a YAC.  
     The following abbreviations are used to  
     associate primary accession  
     numbers given in the feature table with their  
     source databases:  
         Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:,  
         WORMPEP; Information  
         on the WORMPEP database can be found at

SNP  
 UniSTS  
 LinkOut

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep)  
     This sequence was generated from part of  
     bacterial clone contigs of  
     human chromosome 13, constructed by the Sanger  
     Centre Chromosome 13  
     Mapping Group. Further information can be  
     found at <http://www.sanger.ac.uk/HGP/Chrl3>  
         IMPORTANT: This sequence is not the entire  
     insert of clone  
         RP11-313L9. It may be shorter because we  
     sequence overlapping  
         sections only once, except for a short overlap.  
     During sequence assembly data is compared from  
     overlapping clones.  
     Where differences are found these are  
     annotated as variations  
         together with a note of the overlapping clone  
     name. Note that the  
         variation annotation may not be found in the  
     sequence submission  
         corresponding to the overlapping clone, as we  
     submit sequences with  
         only a small overlap.  
     The true right end of clone RP11-358F13 is at  
     100 in this sequence.  
     The true left end of clone RP11-4086 is at  
     100074 in this sequence.  
     The true right end of clone RP11-313L9 is at  
     143409 in this  
         sequence.  
     RP11-313L9 is from the library RPCI-11.2  
     constructed by the group  
         of Pieter de Jong. For further details see  
<http://bacpac.chori.org/>  
     VECTOR: pBACe3.6.

**FEATURES**

<b>source</b>	Location/Qualifiers
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	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:3606"
	/chromosome="13"
	/clone="RP11-313L9"
	/clone_lib="RPCI-11.2"
<b>misc_feature</b>	101..143409
	/note="annotated region of clone"
<b>gene</b>	join
(68116..68379,68867..69026,69792..69841)	/locus_tag="RP11-313L9.1-001"
<b>mRNA</b>	join
(68116..68379,68867..69026,69792..69841)	/locus_tag="RP11-313L9.1-001"
	/product="novel transcript"
	/note="match: ESTs: Em:AW816149.1"
	:complement(93671..126402)
<b>gene</b>	/gene="IRS2"
<b>mRNA</b>	/locus_tag="RP11-313L9.2-001"
	complement(join

4

Priority date : July 29, 2003

E genome containing T<sub>R</sub>S-2 gene

AL 162497 (Version 20 Oct. 3, 2002)

